

SEQUENCE LISTING

<110> Japan Science And Technology Corporation

<120> Nicotianamine synthase, genes coding nicotianamine synthase

<130> PA906235

<160> 22

<210> 1

<211> 328

<212> PRT

<213> Hordeum vulgare L.

<400> 1

Met Asp Ala Gln Asn Lys Glu Val Ala Ala Leu Ile Glu Lys Ile	15
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Ser Pro Glu Val Asp Arg Leu Phe Thr Asp Leu Val Thr Ala Cys	45
Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Ser Pro Glu His	60
Gln Arg Met Arg Glu Ala Leu Ile Arg Leu Cys Ser Ala Ala Glu	75
Gly Lys Leu Glu Ala His Tyr Ala Asp Leu Leu Ala Thr Phe Asp	90
Asn Pro Leu Asp His Leu Gly Leu Phe Pro Tyr Tyr Ser Asn Tyr	105
Val Asn Leu Ser Arg Leu Glu Tyr Glu Leu Leu Ala Arg His Val	120
Pro Gly Ile Ala Pro Ala Arg Val Ala Phe Val Gly Ser Gly Pro	135
Leu Pro Phe Ser Ser Leu Val Leu Ala Ala His His Leu Pro Glu	150
Thr Gln Phe Asp Asn Tyr Asp Leu Cys Gly Ala Ala Asn Glu Arg	165
Ala Arg Lys Leu Phe Gly Ala Thr Ala Asp Gly Val Gly Ala Arg	180
Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Gln Glu Leu	195

Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala	210
Ala Glu Glu Lys Ala Lys Val Ile Ala His Leu Gly Ala His Met	225
Val Glu Gly Ala Ser Leu Val Val Arg Ser Ala Arg Pro Arg Gly	240
Phe Leu Tyr Pro Ile Val Asp Pro Glu Asp Ile Arg Arg Gly Gly	255
Phe Glu Val Leu Ala Val His His Pro Glu Gly Glu Val Ile Asn	270
Ser Val Ile Val Ala Arg Lys Ala Val Glu Ala Gln Leu Ser Gly	285
Pro Gln Asn Gly Asp Ala His Ala Arg Gly Ala Val Pro Leu Val	300
Ser Pro Pro Cys Asn Phe Ser Thr Lys Met Glu Ala Ser Ala Leu	315
Glu Lys Ser Glu Glu Leu Thr Ala Lys Glu Leu Ala Phe	328

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<211> 1295

<212> DNA

<213> *Hordeum vulgare* L.

<400> 2

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130	140	150	160	170	180
GCCGAGCTGC CGTCGCTGAG CCCGTCCCC GAGGTCGACA GGCTCTTCAC CGACCTCGTC					
190	200	210	220	230	240
ACGGCCTGCG TCCCGCCGAG CCCCGTCGAC GTGACGAAGC TCAGCCCGGA GCACCAGAGG					
250	260	270	280	290	300

ATGCGGGAGG CTCTCATCCG CTTGTGCTCC GCCGCCGAGG GGAAGCTCGA GGCGBACTAC

310 320 330 340 350 360
GCCGACCTGC TCGCCACCTT CGACAACCCG CTCGACCACC TCGGCCTCTT CCCGTACTAC

370 380 390 400 410 420
AGCAACTACG TCAACCTCAG CAGGCTGGAG TACGAGCTCC TGGCGCGCCA CGTGCCGGGC

430 440 450 460 470 480
ATCGCGCCGG CGCGCGTCGC CTTGCTCGGC TCCGGCCCCG TGCCGTTTCA CTCGCTCGTC

490 500 510 520 530 540
CTCGCCGCGC ACCACCTGCC CGAGACCCAG TTCGACAAC TACGACCTGTG CGGCGCGGCC

550 560 570 580 590 600
AACGAGCGCG CCAGGAAGCT GTTCGGCGCG ACGGCGGACG GCGTCGGCGC GCGTATGTGC

610 620 630 640 650 660
TTCCACACGG CGGACGTCGC CGACCTCACC CAGGAGCTCG GCGCCTACGA CGTGGTCTTC

670 680 690 700 710 720
CTCGCCGCGC TCGTCGGCAT GGCAGCCGAG GAGAAGGCCA AGGTGATTGC CCACCTGGGC

730 740 750 760 770 780
GCGCACATGG TGGAGGGGGC GTCCCTGGTC GTGCGGAGCG CACGGCCCCG CGGCTTTCTT

790 800 810 820 830 840
TACCCCATTTG TCGACCCGGA GGACATCAGG CGGGGTGGGT TCGAGGTGCT GGCCGTGCAC

850	860	870	880	890	900
CACCCGGAAG GTGAGGTGAT CAACTCTGTC ATCGTCGCCC GTAAGGCCGT CGAAGCGCAG					
910	920	930	940	950	960
CTCAGTGGGC CGCAGAACGG AGACGCGCAC GCACGGGGCG CGGTGCCGTT GGTCAGCCCG					
970	980	990	1000	1010	1020
CCATGCAACT TCTCCACCAA GATGGAGGCG AGCGCGCTTG AGAAGAGCGA GGAGCTGACC					
1030	1040	1050	1060	1070	1080
GCCAAAGAGC TGGCCTTTTG ATTGAAGAGT GCGCGTGGTC ATTCTGTCGC CTGCGATCGT					
1090	1100	1110	1120	1130	1140
GGTAACTTTC CTACTCGTGT GTGTTTTGAT GTTTGTGCCT GTAAGAGTTA TGCTTCCGGC					
1150	1160	1170	1180	1190	1200
CTTGTGCTGT TAATTTACAC GCGTTACATG TAGTACTTGT ATTTATACCT GGAATAACGG					
1210	1220	1230	1240	1250	1260
TATGTAAACAT AAATATTAGT GGGATTTGAA GTGTAATGCT AAATAATAAG AAAACTTGAT					
1270	1280	1290	1300		
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<210> 3

<211> 335

<212> PRT

<213> *Hordeum vulgare* L.

<400> 3

Met Ala Ala Gln Asn Asn Gln Glu Val Asp Ala Leu Val Glu Lys	15
Ile Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser	30
Pro Ser Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr Ala	45
Cys Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu	60
Ala Gln Glu Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala	75
Glu Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe	90
Asp Lys Pro Leu Asp His Leu Gly Met Phe Pro Tyr Tyr Asn Asn	105
Tyr Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg Tyr	120
Val Pro Gly Gly Tyr Arg Pro Ala Arg Val Ala Phe Ile Gly Ser	135
Gly Pro Leu Pro Phe Ser Ser Phe Val Leu Ala Ala Arg His Leu	150
Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu Cys Gly Ala Ala Asn	165
Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Arg Asp Val Gly Ala	180
Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Ala Gly Glu	195
Leu Ala Lys Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met	210
Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala His	225
Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala His Gly Ala	240
Arg Gly Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg	255
Gly Gly Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val	270
Val Asn Ser Val Ile Ile Ala Gln Lys Ser Lys Asp Val His Ala	285
Asp Gly Leu Gly Ser Gly Arg Gly Ala Gly Gly Gln Tyr Ala Arg	300
Gly Thr Val Pro Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met	315
Val Ala Asp Val Thr Gln Asn His Lys Arg Asp Glu Phe Ala Asn	330
Ala Glu Val Ala Phe	335

<210> 4

<211> 1342

<212> DNA

<213> *Hordeum vulgare* L.

<400> 4

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70	80	90	100	110	120
GAGGTGGATG	CCCTGGTGGA	GAAGATCACC	GGGCTCCATG	CCGCAATCGC	CAAGCTGCCG
130	140	150	160	170	180
TCGCTCAGCC	CATCCCCGGA	CGTCGACGCG	CTCTTCACGG	AGCTGGTCAC	GGCGTGCGTT
190	200	210	220	230	240
CCACCGAGTC	CAGTGGACGT	GACCAAGCTC	GGGCCGGAGG	CGCAGGAGAT	GCGGGAGGGC
250	260	270	280	290	300
CTCATCCGCC	TATGCTCCGA	GGCCGAGGGG	AAGCTGGAGG	CGCACTACTC	CGACATGCTC
310	320	330	340	350	360
GCCGCCTTCG	ACAAGCCGCT	GGATCACCTC	GGCATGTTCC	CCTACTACAA	CAACTACATC
370	380	390	400	410	420
AACCTCAGCA	AGCTCGAGTA	CGAGCTCCTG	GCCCGCTACG	TGCCTGGCGG	CTATCGCCCG
430	440	450	460	470	480
GCGCGCGTCG	CGTTCATCGG	CTCCGGCCCCG	CTGCCGTTCA	GCTCCTTTGT	CCTGGCCGCG
490	500	510	520	530	540

CGCCACCTGC CCGACACCAT GTTCGACAAC TATGACCTGT GCGGTGCGGC CAACGATCGC

550 560 570 580 590 600
GCCAGCAAGC TCTTCGCGC GGATCGCGAC GTGGGTGCCC GCATGTCGTT CCACACGGCC

610 620 630 640 650 660
GACGTGCGCG ACCTCGCCGG CGAGCTCGCC AAGTACGACG TTGTCTTCCT GGCCGCACTC

670 680 690 700 710 720
GTCGGCATGG CCGCCGAGGA CAAGGCGAAG GTGATCGCGC ACCTCGGCGC ACACATGGCA

730 740 750 760 770 780
GACGGGGCGG CCCTCGTCGT GCGCAGCGCA CACGGAGCGC GCGGGTTCCT GTACCCGATC

790 800 810 820 830 840
GTCGACCCCC AGGACATCGG CCGAGGCGGG TTCGAGGTGC TGGCCGTGTG CCATCCCGAC

850 860 870 880 890 900
GACGACGTGG TGAACTCCGT CATCATCGCA CAGAAGTCCA AGGACGTGCA TGCCGATGGA

910 920 930 940 950 960
CTTGGCAGCG GGC GTGGTGC CGGTGGACAG TACGCGCGG GCACGGTGCC TGTTGTCAGC

970 980 990 1000 1010 1020
CCCCCGTGCA GGTTCGGCGA GATGGTGGCG GACGTGACCC AGAACCACAA GAGAGACGAG

1030 1040 1050 1060 1070 1080
TTTGCCAACG CCGAAGTGGC CTTTGTGATCG TTCGCTGCGA GGGTGTGCAT CCATGATCCA

1090	1100	1110	1120	1130	1140
TCCATACCTC GTTCTGTGAT TGCATCAAGC TTGCAATCGT ATGCATTTC AAGTCACGTGT					
1150	1160	1170	1180	1190	1200
TGCTTCTATC CAATAATGTA CGTGTGGTGT TTACACGCGA ATGTCTTGTA GACCTTTGTA					
1210	1220	1230	1240	1250	1260
TGTGTACAAG TGAATTTTAA TTCACAAGTA CATATAATGG TCACCATTGA AAAGATGTTT					
1270	1280	1290	1300	1310	1320
AGTGTGTGTT TTCCAATATA TGTTTGTGTA AGGTTTCATCA TCTAATAAAA TATGTTTGGA					
1330	1340	1350			
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<210> 5

<211> 335

<212> PRT

<213> *Hordeum vulgare* L.

<400> 5

Met Ala Ala Gln Asn Asn Asn Lys Asp Val Ala Ala Leu Val Glu	15
Lys Ile Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu	30
Ser Pro Ser Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr	45
Ala Cys Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro	60
Glu Ala Gln Glu Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu	75
Ala Glu Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala	90
Phe Asp Asn Pro Leu Asp His Leu Gly Ile Phe Pro Tyr Tyr Ser	105

Asn Tyr Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg	120
Tyr Val Arg Arg His Arg Pro Ala Arg Val Ala Phe Ile Gly Ser	135
Gly Pro Leu Pro Phe Ser Ser Phe Val Leu Ala Ala Arg His Leu	150
Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu Cys Gly Ala Ala Asn	165
Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Thr Asp Val Gly Ala	180
Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Ala Ser Glu	195
Leu Ala Lys Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met	210
Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala His	225
Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala His Gly Ala	240
Arg Gly Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg	255
Gly Gly Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val	270
Val Asn Ser Val Ile Ile Ala Gln Lys Ser Lys Glu Val His Ala	285
Asp Gly Leu Gly Ser Ala Arg Gly Ala Gly Arg Gln Tyr Ala Arg	300
Gly Thr Val Pro Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met	315
Val Ala Asp Val Thr Gln Asn His Lys Arg Asp Glu Phe Ala Asn	330
Ala Glu Val Ala Phe	335

<210> 6

<211> 1314

<212> DNA

<213> *Hordeum vulgare* L.

<400> 6

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70	80	90	100	110	120
AGGATGTCGC TGCCCTGGTG GAGAAGATCA CCGGGCTCCA CGCCGCCATC GCCAAGCTGC					

130	140	150	160	170	180
CGTCGCTCAG	CCCATCCCCG	GACGTCGACG	CGCTCTTCAC	CGAGCTGGTC	ACGGCGTGCG
190	200	210	220	230	240
TTCCCCCGAG	CCCCGTGGAC	GTGACCAAGC	TCGGCCCCGA	GGCGCAGGAG	ATGCGGGAGG
250	260	270	280	290	300
GCCTCATCCG	CCTCTGCTCC	GAGGCCGAGG	GGAAGCTGGA	GGCGCACTAC	TCCGACATGC
310	320	330	340	350	360
TCGCCGCCTT	CGACAACCCG	CTGGATCACC	TCGGCATCTT	CCCCTACTAC	AGCAACTACA
370	380	390	400	410	420
TCAACCTCAG	CAAGCTGGAG	TACGAGCTCC	TGGCACGCTA	CGTCCGGCGG	CATCGCCCGG
430	440	450	460	470	480
CCCGCGTCGC	GTTTCATCGGC	TCCGGCCCCG	TGCCGTTTCT	CTCCTTTGTC	CTGGCCGCGC
490	500	510	520	530	540
GCCACCTGCC	CGACACCATG	TTTGACAACT	ACGACCTTTG	CGGCGCGGCC	AACGATCGCG
550	560	570	580	590	600
CCAGCAAGCT	CTTCCGCGCG	GACACGGACG	TGGGTGCCCC	CATGTCGTTT	CACACGGCCG
610	620	630	640	650	660
ACGTCGCGGA	CCTCGCCAGC	GAGCTCGCCA	AGTACGACGT	CGTCTTCCTG	GCCGCGCTCG
670	680	690	700	710	720
TCGGCATGGC	CGCCGAGGAC	AAGGCCAAGG	TGATCGCGCA	CCTCGGCGCA	CACATGGCAG

730 740 750 760 770 780
ACGGGGCGGC CCTCGTCGTG CGCAGCGCAC ACGGAGCGCG CGGGTTCCTG TACCCGATTG

790 800 810 820 830 840
TCGACCCCCA GGACATCGGC CGCGGCGGGT TCGAGGTGCT GGCCGTGTGC CACCCCGACG

850 860 870 880 890 900
ACGACGTGGT GAACTCCGTC ATCATCGCAC AGAAGTCCAA GGAGGTGCAT GCCGATGGAC

910 920 930 940 950 960
TTGGCAGCGC GCGTGGTGCC GGTGACAGT ACGCGCGCGG CACGGTGCCG GTTGTCAGCC

970 980 990 1000 1010 1020
CCCCGTGCAG GTTCGGTGAG ATGGTGGCGG ATGTGACCCA GAACCACAAG AGAGACGAGT

1030 1040 1050 1060 1070 1080
TTGCCAACGC CGAAGTGGCC TTTTGATCGA TCGTCGCCAA GGGACAATAA ATGAACGTGG

1090 1100 1110 1120 1130 1140
ATGTGGTAGG GTAATTTGCC TACCTCGCTG CTTGATCGCT TGCAATATGT GCACATTTTC

1150 1160 1170 1180 1190 1200
CTACTACCGC TGCTTATGCA TTTCAAGCCA TGTGATGTTG GTATCCAATA AAGTATGTGT

1210 1220 1230 1240 1250 1260
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1270 1280 1290 1300 1310 1320

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<210> 7

<211> 329

<212> PRT

<213> Hordeum vulgare L.

<400> 7

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Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro	30
Ser Pro Asp Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys	45
Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Ala Pro Glu Ala	60
Gln Ala Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu	75
Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp	90
Asn Pro Leu Asp His Leu Gly Val Phe Pro Tyr Tyr Ser Asn Tyr	105
Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg Tyr Val	120
Pro Gly Arg His Arg Pro Ala Arg Val Ala Phe Ile Gly Ser Gly	135
Pro Leu Pro Phe Ser Ser Tyr Val Leu Ala Ala Arg His Leu Pro	150
Asp Thr Val Phe Asp Asn Tyr Asp Leu Cys Gly Ala Ala Asn Asp	165
Arg Ala Thr Arg Leu Phe Arg Ala Asp Lys Asp Val Gly Ala Arg	180
Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Asp Glu Leu	195
Ala Thr Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala	210
Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala His Met	225
Ala Asp Gly Ala Ala Leu Val Ala Arg His Gly Ala Arg Gly Phe	240
Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly Gly Phe	255
Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn Ser	270
Val Ile Ile Ala Gln Lys Ser Asn Asp Val His Glu Tyr Gly Leu	285
Gly Ser Gly Arg Gly Gly Arg Tyr Ala Arg Gly Thr Val Val Pro	300

Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val	315
Thr Gln Lys Arg Glu Glu Phe Ala Asn Ala Glu Val Ala Phe	329

<210> 8

<211> 1249

<212> DNA

<213> *Hordeum vulgare* L.

<400> 8

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70	80	90	100	110	120
ACATAAAAAT	GGACGGCCAG	AGCGAGGAGG	TCGACGCCCT	TGTCCAGAAG	ATCACCGGCC
130	140	150	160	170	180
TCCACGCCGC	CATCGCCAAG	CTGCCCTCGC	TCAGCCCGTC	CCCGGACGTC	GACGCGCTCT
190	200	210	220	230	240
TCACCGACCT	GGTCACCGCG	TGCGTGCCCC	CGAGCCCCGT	GGACGTGACC	AAGCTCGCCC
250	260	270	280	290	300
CGGAGGCGCA	GGCGATGCGG	GAGGGCCTCA	TCCGCCTCTG	CTCCGAGGCC	GAGGGCAAGC
310	320	330	340	350	360
TGGAGGCGCA	CTACTCCGAC	ATGCTCGCCG	CCTTCGACAA	CCCGCTCGAC	CACCTCGGCG
370	380	390	400	410	420
TCTTCCCCTA	CTACAGCAAC	TACATCAACC	TCAGCAAGCT	TGAGTACGAG	CTCCTCGCGC

430 440 450 460 470 480
GCTACGTGCC CGGCAGGCAT CGCCCGGCCC GCGTCGCCTT CATCGGCTCC GGCCCGCTGC

490 500 510 520 530 540
CGTTCAGCTC CTACGTCCTC GCCGCGCGCC ACCTGCCCGA CACCGTGTTT GACAACTACG

550 560 570 580 590 600
ACCTGTGCGG CGCGGCCAAC GACCGCGCGA CCAGGCTGTT CCGCGCGGAC AAGGACGTCG

610 620 630 640 650 660
GCGCCCGCAT GTCGTTCCAC ACCGCCGACG TCGCGGACCT CACCGACGAG CTCGCTACGT

670 680 690 700 710 720
ACGACGTCGT CTTCTGGGCC GCGCTCGTGG GCATGGCCGC CGAGGACAAG GCCAAGGTGA

730 740 750 760 770 780
TCGCGCACCT TGGCGCGCAC ATGGCGGACG GGGCGGCCCT CGTTGCGCGG CACGGCGCGC

790 800 810 820 830 840
GTGGGTTTCT CTACCCGATC GTCGATCCCC AGGACATCGG TCGAGGCGGG TTCGAGGTGC

850 860 870 880 890 900
TCGCCGTGTG TCACCCCGAC GACGACGTGG TGAATCCGT CATCATCGCA CAAAAGAGCA

910 920 930 940 950 960
ACGACGTGCA CGAGTATGGA CTTGGCAGCG GCGTGTTGG ACGGTACGCG CGAGGCACGG

970 980 990 1000 1010 1020

TGGTGCCGGT GGTGAGCCCA CCCTGCAGGT TCGGCGAGAT GGTGGCAGAC GTGACCCAGA

1030 1040 1050 1060 1070 1080
AGAGAGAGGA GTTTGCCAAC GCGGAAGTGG CCTTCTGATT GCTGCTGAAT CGCTTGTGAT

1090 1100 1110 1120 1130 1140
CGTACGTGGT AATTTTTCTA CTACTCCTCC TCCTACCACC ACCTATCACC TATGTATGCA

1150 1160 1170 1180 1190 1200
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1210 1220 1230 1240 1250
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<210> 9

<211> 282

<212> PRT

<213> *Hordeum vulgare* L.

<400> 9

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Thr Gly Leu His Ala Ala Ile Ser Lys Leu Pro Ala Leu Ser Pro	30
Ser Pro Gln Val Asp Ala Leu Phe Thr Glu Leu Val Ala Ala Cys	45
Val Pro Ser Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu Ala	60
Gln Glu Met Arg Gln Asp Leu Ile Arg Leu Cys Ser Ala Ala Glu	75
Gly Leu Leu Glu Ala His Tyr Ser Asp Met Leu Thr Ala Leu Asp	90
Ser Pro Leu Asp His Leu Gly Arg Phe Pro Tyr Phe Asp Asn Tyr	105
Val Asn Leu Ser Lys Leu Glu His Asp Leu Leu Ala Gly His Val	120

Ala Ala Pro Ala Arg Val Ala Phe Ile Gly Ser Gly Pro Leu Pro	135
Phe Ser Ser Leu Phe Leu Ala Thr Tyr His Leu Pro Asp Thr Arg	150
Phe Asp Asn Tyr Asp Arg Cys Ser Val Ala Asn Gly Arg Ala Met	165
Lys Leu Val Gly Ala Ala Asp Glu Gly Val Arg Ser Arg Met Ala	180
Phe His Thr Ala Glu Val Thr Asp Leu Thr Ala Glu Leu Gly Ala	195
Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Thr Ser Lys	210
Glu Lys Ala Asp Ala Ile Ala His Leu Gly Lys His Met Ala Asp	225
Gly Ala Val Leu Val Arg Glu Ala Leu His Gly Ala Arg Ala Phe	240
Leu Tyr Pro Val Val Glu Leu Asp Asp Val Gly Arg Gly Gly Phe	255
Gln Val Leu Ala Val His His Pro Ala Gly Asp Glu Val Phe Asn	270
Ser Phe Ile Val Ala Arg Lys Val Lys Met Ser Ala	282

<210> 10

<211> 1044

<212> DNA

<213> Hordeum vulgare L.

<400> 10

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ACGCCGCCAT CTCCAAGCTC CCGGCACTAA GCCCGTCTCC TCAAGTCGAC GCGCTCTTCA					
130	140	150	160	170	180
CCGAGCTGGT TCGGGCGTGC GTCCCATCAA GCCCGGTGGA CGTGACCAAG CTCGGCCCGG					
190	200	210	220	230	240
AGGCGCAGGA GATGCGGCAG GACCTCATCC GTCTCTGCTC GGCCGCCGAG GGGCTGCTCG					

250 260 270 280 290 300
AGGCGCACTA CTCCGACATG CTCACCGCGT TGGACAGCCC GCTCGACCAC CTCGGCCGCT

310 320 330 340 350 360
TCCCTTACTT CGACAACCTAC GTCAACCTCA GCAAGCTCGA GCACGATCTT CTGGCAGGTC

370 380 390 400 410 420
ACGTGGCGGC CCCGGCCCCG GTGGCGTTCA TCGGGTCGGG GCCACTGCCG TTCAGCTCGC

430 440 450 460 470 480
TCTTCCTTGC GACGTACCAC CTGCCGGACA CCCGGTTCGA CAACTACGAC CGGTGCAGCG

490 500 510 520 530 540
TGGCGAATGG CCGGGCGATG AAGCTGGTCG GCGCGGCGGA CGAGGGCGTG CGATCACGCA

550 560 570 580 590 600
TGGCGTTCCA CACGGCCGAA GTCACGGACC TCACGGCTGA GCTCGGCGCT TACGACGTGG

610 620 630 640 650 660
TCTTCCTGGC CGCGCTCGTG GGAATGACGT CCAAGGAGAA GGCCGACGCC ATAGCGCACT

670 680 690 700 710 720
TGGGGAAGCA CATGGCAGAT GGGGCGGTGC TCGTGCGCGA AGCGCTGCAC GGGGCGCGAG

730 740 750 760 770 780
CGTTCCTGTA TCCTGTCTGT GAGCTGGACG ATGTCGGGCG TGGTGGGTTC CAAGTGCTGG

790 800 810 820 830 840

CCGTGCACCA CCCTGCAGGC GATGAGGTGT TCAACTCATT CATAGTTGCC CGGAAGGTGA

850 860 870 880 890 900
AAATGAGTGC TTAAATTAAG AAAAGGGTGA GCCTGTCTGC TTGTGCAAAT GGTGTCTCAC

910 920 930 940 950 960
ATTGATAATA ACCAGATGAT ACCCTGCACA TTGATGGGGG TACTGCAGTA TGTTTCAATG

970 980 990 1000 1010 1020
AGGTCTGGTT GTATCAAATA TGAGTATTG GCTTAATAAT ATCAGCGAAT ATGTTTCGAT

1030 1040 1050
TAAAAAAAAA AAAAAAAAAA AAAA

<210> 11

<211> 328

<212> PRT

<213> Hordeum vulgare L.

<400> 11

Met Asp Ala Gln Asn Lys Glu Val Asp Ala Leu Val Gln Lys Ile	15
Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro	30
Ser Pro Asp Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys	45
Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Ser Glu Ala	60
Gln Glu Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu	75
Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp	90
Asn Pro Leu Asp His Leu Gly Met Phe Pro Tyr Tyr Ser Asn Tyr	105
Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg Tyr Val	120
Pro Gly Gly Ile Ala Arg Pro Ala Val Ala Phe Ile Gly Ser Gly	135

Pro Leu Pro Phe Ser Ser Tyr Val Leu Ala Ala Arg His Leu Pro	150
Asp Ala Met Phe Asp Asn Tyr Asp Leu Cys Ser Ala Ala Asn Asp	165
Arg Ala Ser Lys Leu Phe Arg Ala Asp Lys Asp Val Gly Ala Arg	180
Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Arg Glu Leu	195
Ala Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala	210
Ala Glu Asp Lys Ala Lys Val Ile Pro His Leu Gly Ala His Met	225
Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala Gln Ala Arg Gly	240
Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly Gly	255
Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn	270
Ser Val Ile Ile Ala His Lys Ser Lys Asp Val His Ala Asn Glu	285
Arg Pro Asn Gly Arg Gly Gly Gln Tyr Arg Gly Ala Val Pro Val	300
Val Ser Pro Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val Thr	315
His Lys Arg Glu Glu Phe Thr Asn Ala Glu Val Ala Phe	328

<210> 12

<211> 1352

<212> DNA

<213> *Hordeum vulgare* L.

<400> 12

10	20	30	40	50	60
CTCCAATTCTG CTCCTGTGCC TCAGGTAGCC ACAACATACA GTATTAAAAT GGATGCCCAG					
70	80	90	100	110	120
AACAAGGAGG TTGATGCCCT GGTCCAGAAG ATCACCGGCC TCCACGCCGC CATCGCCAAG					
130	140	150	160	170	180
CTGCCGTCCC TCAGCCCATC ACCCGACGTC GACGCGCTCT TCACCGACCT GGTCACCGCG					

190	200	210	220	230	240
TGCGTCCCCC	CGAGCCCCGT	GGACGTGACC	AAGCTCGGGT	CGGAGGCGCA	GGAGATGCGG
250	260	270	280	290	300
GAGGGCCTCA	TCCGCCTCTG	CTCCGAGGCC	GAGGGGAAGC	TGGAGGCGCA	CTACTCCGAC
310	320	330	340	350	360
ATGCTGGCCG	CCTTCGACAA	CCCGCTCGAC	CACCTCGGCA	TGTTCCCCTA	CTACAGCAAC
370	380	390	400	410	420
TACATCAACC	TCAGCAAGCT	GGAGTACGAG	CTCCTGGCGC	GCTACGTGCC	GGGCGGCATC
430	440	450	460	470	480
GCCCCGGCCG	CTGTCGCGTT	CATCGGCTCC	GGCCCCGCTGC	CGTTCAGCTC	CTACGTCCTC
490	500	510	520	530	540
GCCGCTCGCC	ACCTGCCCCG	CGCCATGTTC	GACAACTACG	ACCTGTGTAG	CGCGGCCAAC
550	560	570	580	590	600
GACCGTGCGA	GCAAGCTGTT	CCGCGCGGAC	AAGGACGTGG	GCGCCCGCAT	GTCTTTCCAC
610	620	630	640	650	660
ACCGCCGACG	TAGCGGACCT	CACCCGCGAG	CTCGCCGCGT	ACGACGTCGT	CTTCCTGGCC
670	680	690	700	710	720
GCGCTCGTGG	GCATGGCTGC	CGAGGACAAG	GCCAAGGTGA	TTCCGCACCT	CGGCGCGCAC
730	740	750	760	770	780

ATGGCGGACG GGGCGGCCCT CGTCGTGCGC AGTGCGCAGG CACGTGGGTT CCTCTACCCG

790 800 810 820 830 840
ATCGTCGATC CCCAGGACAT CGGTCGAGGC GGGTTTGAGG TGCTGGCCGT GTGTCACCCC

850 860 870 880 890 900
GACGATGACG TGGTGAAGTC CGTCATCATC GCACACAAGT CCAAGGACGT GCATGCCAAT

910 920 930 940 950 960
GAACGTCCCA ACGGGCGTGG TGGACAGTAC CGGGGCGCGG TACCGGTGGT CAGCCCGCCG

970 980 990 1000 1010 1020
TGCAGGTTCG GTGAGATGGT GGC GGACGTG ACCCACAAGA GAGAGGAGTT CACCAACGCG

1030 1040 1050 1060 1070 1080
GAAGTGGCCT TCTGATCGTT GCGAGGGAAT GAAAATGAAG GTGGACGTGT GTGGTCAGCA

1090 1100 1110 1120 1130 1140
TCCATACGTG GCTGCCTGCT TCATCGCTTG CAATCGTACT ACTACCTACC TATGCAGTTC

1150 1160 1170 1180 1190 1200
AAGTCATGTG TTGTCAATGT AAGTGTGATG TTTACACTAG TCTATGAAAG GCAGGGCAGA

1210 1220 1230 1240 1250 1260
CGAGGGTAGT GTGCCAAGTA ACAGTGTGTC ATTATAGGTG TAAGTGTTGA GAATAAGACC

1270 1280 1290 1300 1310 1320
ATTTTTGTTC ACAAATAGTA TGATGTAATC GGTGTCATAT TCGTATTGAG TACATTTGTC

1330

1340

1350

1360

AAGTTGGTTG CTAAAAAAAA AAAAAAAAAA AA

<210> 13

<211> 329

<212> PRT

<213> Hordeum vulgare L.

<400> 13

Met Asp Ala Gln Ser Lys Glu Val Asp Ala Leu Val Gln Lys Ile	15
Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro	30
Ser Pro Asp Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys	45
Val Pro Pro Ser Pro Val Asp Val Thr Lys Leu Ala Pro Glu Ala	60
Gln Ala Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu	75
Gly Lys Leu Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp	90
Asn Pro Leu Asp His Leu Gly Val Phe Pro Tyr Tyr Ser Asn Tyr	105
Ile Asn Leu Ser Lys Leu Glu Tyr Glu Leu Leu Ala Arg Tyr Val	120
Pro Gly Gly Ile Ala Pro Ala Arg Val Ala Phe Ile Gly Ser Gly	135
Pro Leu Pro Phe Ser Ser Tyr Val Leu Ala Ala Arg His Leu Pro	150
Asp Thr Val Phe Asp Asn Tyr Val Pro Val Arg Ala Ala Asn Asp	165
Arg Ala Thr Arg Leu Phe Arg Ala Asp Lys Asp Val Gly Ala Arg	180
Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Asp Glu Leu	195
Ala Thr Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala	210
Ala Glu Asp Lys Gly Gln Gly Asp Pro His Leu Gly Ala His Met	225
Ala Asp Gly Ala Ala Leu Val Arg Ser Ala His Gly Ala Arg Gly	240
Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly Gly	255
Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn	270
Ser Val Ile Ile Ala Gln Lys Ser Lys Asp Met Phe Ala Asn Gly	285

Pro Arg Asn Gly Cys Gly Gly Arg Tyr Ala Arg Gly Thr Val Pro	300
Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val	315
Thr Gln Lys Arg Glu Glu Phe Ala Lys Ala Glu Val Ala Phe	329

<210> 14

<211> 1371

<212> DNA

<213> Hordeum vulgare L.

<400> 14

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AGCTCATCAC	TGGTCAGGTA	CCAAGAAGAC	ATAAAAATGG	ACGCCCAGAG
110	120	130	140	150
CAAGGAGGTC	GACGCCCTTG	TCCAGAAGAT	CACCGGCCTC	CACGCCGCCA
160	170	180	190	200
TCGCCAAGCT	GCCCTCGCTC	AGCCCGTCCC	CGGACGTCGA	CGCGCTCTTC
210	220	230	240	250
ACCGACCTGG	TCACCGCGTG	CGTGCCCCCG	AGCCCGGTGG	ACGTGACCAA
260	270	280	290	300
GCTCGCCCCG	GAGGCGCAGG	CGATGCGGGA	GGGCCTCATC	CGCCTCTGCT
310	320	330	340	350
CCGAGGCCGA	GGGCAAGCTG	GAGGCGCACT	ACTCCGACAT	GCTCGCCGCC
360	370	380	390	400
TTCGACAACC	CGCTCGACCA	CCTCGGCGTC	TTCCCCTACT	ACAGCAACTA
410	420	430	440	450

CATCAACCTC	AGCAAGCTCG	AGTACGAGCT	CCTCGCGCGC	TACGTGCCCCG
460	470	480	490	500
GCGGCATCGC	CCCGGCCCGC	GTCGCCTTCA	TCGGCTCCGG	CCCGCTCCCG
510	520	530	540	550
TTCAGCTCCT	ACGTCCTCGC	CGCGCGCCAC	CTGCCCCGACA	CCGTGTTTCA
560	570	580	590	600
CAACTACGTA	CCTGTGCGCG	CGGCCAACGA	CCGCGCGACC	AGGCTGTTCC
610	620	630	640	650
GCGCGGACAA	GGACGTCGGC	GCCCGCATGT	CGTTCCACAC	CGCCGACGTC
660	670	680	690	700
GCGGACCTCA	CCGACGAGCT	CGCTACGTAC	GACGTCGTCT	TCCTGGCCGC
710	720	730	740	750
GCTCGTGGGC	ATGGCCGCCG	AGGACAAGGG	CCAAGGTGAT	CCGCACCTTG
760	770	780	790	800
GCGCGCACAT	GGCGGACGGG	GCGGCCCTCG	TCCGCAGCGC	GCACGGGGCG
810	820	830	840	850
CGTGGGTTCC	TCTACCCGAT	CGTCGATCCC	CAAGACATTG	GTCGAGGCGG
860	870	880	890	900
GTTCGAGGTG	CTCGCCGTGT	GTCACCCCGA	CGACGACGTG	GTGAACTCCG
910	920	930	940	950
TCATCATCGC	GCAGAAGTCT	AAGGACATGT	TTGCCAATGG	ACCTCGCAAC
960	970	980	990	1000
GGGTGTGGTG	GACGGTACGC	GCGAGGCACG	GTGCCGGTGG	TCAGCCCGCC
1010	1020	1030	1040	1050
CTGCAGGTTT	GGCGAGATGG	TGGCAGACGT	GACCCAGAAG	AGAGAGGAGT
1060	1070	1080	1090	1100
TTGCCAAGGC	GGAAGTGGCC	TTCTGATTGC	TGCGAGGTCA	CCATCCGTAT
1110	1120	1130	1140	1150
GCCGCTGCTA	CCTTTCAATA	TCTTGCAATC	GTAGGTGGCG	ATTTTCCTAC

1160	1170	1180	1190	1200
TCTTGTTACG	ACCTTTCAAA	TCATATGTTG	TTTGTACCCA	ATAATGTAAG
1210	1220	1230	1240	1250
TGTGTTGCTT	ACACGCGCAT	GTCTTGTACA	CTCGGTCTCT	AGAAGGCAGG
1260	1270	1280	1290	1300
GCAGATCAAG	AGACTGTGCA	AAGGAAAAGA	AATGTGTGTT	GTTGTAGGTG
1310	1320	1330	1340	1350
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1360	1370	1380		
AAAAAAAAAA	AAAAAAAAAA	A		

<210> 15

<211> 332

<212> PRT

<213> *Oryza sativa* L.

<400> 15

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Ser Ala Glu Val Asp Ala Leu Phe Thr Asp Leu Val Thr Ala Cys	45
Val Pro Ala Ser Pro Val Asp Val Ala Lys Leu Gly Pro Glu Ala	60
Gln Ala Met Arg Glu Glu Leu Ile Arg Leu Cys Ser Ala Ala Glu	75
Gly His Leu Glu Ala His Tyr Ala Asp Met Leu Ala Ala Phe Asp	90
Asn Pro Leu Asp His Leu Ala Arg Phe Pro Tyr Tyr Gly Asn Tyr	105
Val Asn Leu Ser Lys Leu Glu Tyr Asp Leu Leu Val Arg Tyr Val	120
Pro Gly Ile Ala Pro Thr Arg Val Ala Phe Val Gly Ser Gly Pro	135
Leu Pro Phe Ser Ser Leu Val Leu Ala Ala His His Leu Pro Asp	150

Ala Val Phe Asp Asn Tyr Asp Arg Cys Gly Ala Ala Asn Glu Arg	165
Ala Arg Arg Leu Phe Arg Gly Ala Asp Glu Gly Leu Gly Ala Arg	180
Met Ala Phe His Thr Ala Asp Val Ala Thr Leu Thr Gly Glu Leu	195
Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Ala	210
Ala Glu Glu Lys Ala Gly Val Ile Ala His Leu Gly Ala His Met	225
Ala Asp Gly Ala Ala Leu Val Val Arg Thr Ala His Gly Ala Arg	240
Gly Phe Leu Tyr Pro Ile Val Asp Pro Glu Asp Val Arg Arg Gly	255
Gly Phe Asp Val Leu Ala Val Cys His Pro Glu Asp Glu Val Ile	270
Asn Ser Val Ile Val Ala Arg Lys Val Gly Ala Ala Ala Ala Ala	285
Ala Ala Ala Arg Arg Asp Glu Leu Ala Asp Ser Arg Gly Val Val	300
Leu Pro Val Val Gly Pro Pro Ser Thr Cys Cys Lys Val Glu Ala	315
Ser Ala Val Glu Lys Ala Glu Glu Phe Ala Ala Asn Lys Glu Leu	330
Ser Val*	345

<210> 16

<211> 1372

<212> DNA

<213> *Oryza sativa* L.

<400> 16

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TCAGCTCACT	CGTGTTCCCA	ACCGCGACAA	AGCTTCACAG	ATGGAGGCTC
110	120	130	140	150
AGAACCAAGA	GGTCGCTGCC	CTGGTCGAGA	AGATCGCCGG	CCTCCACGCC
160	170	180	190	200

GCCATCTCCA	AGCTGCCGTC	GCTGAGCCCA	TCCGCCGAGG	TGGACGCGCT
210	220	230	240	250
CTTACCGAC	CTCGTCACGG	CGTGCGTCCC	GGCGAGCCCC	GTCGACGTGG
260	270	280	290	300
CCAAGCTCGG	CCCGGAGGCG	CAGGCGATGC	GGGAGGAGCT	CATCCGCCTC
310	320	330	340	350
TGCTCCGCCG	CCGAGGGCCA	CCTCGAGGCG	CACTACGCCG	ACATGCTCGC
360	370	380	390	400
CGCCTTCGAC	AACCCGCTCG	ACCACCTCGC	CCGCTTCCCG	TACTACGGCA
410	420	430	440	450
ACTACGTCAA	CCTGAGCAAG	CTGGAGTACG	ACCTCCTCGT	CCGCTACGTC
460	470	480	490	500
CCCGGCATTG	CCCCCACCCG	CGTCGCCTTC	GTCGGGTCGG	GCCCGCTGCC
510	520	530	540	550
GTTCAGCTCC	CTCGTGCTCG	CTGCGCACCA	CCTGCCGGAC	GCGGTGTTCG
560	570	580	590	600
ACAACCTACGA	CCGGTGCGGC	GCGGCCAACG	AGCGGGCGAG	GAGGCTGTTC
610	620	630	640	650
CGCGGCGCCG	ACGAGGGCCT	CGGCGCGCGC	ATGGCGTTCC	ACACCGCCGA
660	670	680	690	700
CGTGCGGACC	CTGACGGGGG	AGCTCGGCGC	GTACGACGTC	GTGTTCTTGG
710	720	730	740	750
CGGCGCTCGT	GGGCATGGCG	GCCGAGGAGA	AGGCCGGGGT	GATCGCGCAC
760	770	780	790	800
CTGGGCGCGC	ACATGGCGGA	CGGCGCGGCG	CTCGTCGTGC	GGACGGCGCA
810	820	830	840	850
CGGGGCGCGC	GGGTTCCTGT	ACCCGATCGT	CGATCCCGAG	GACGTCAGGC
860	870	880	890	900
GTGGCGGGTT	CGACGTTCTG	GCGGTGTGCC	ACCCGGAGGA	CGAGGTGATC

910	920	930	940	950
AACTCCGTCA	TCGTCGCCCCG	CAAGGTCGGT	GCCGCCGCCG	CCGCCGCCGC
960	970	980	990	1000
GGCGCGCAGA	GACGAGCTCG	CGGACTCGCG	CGGCGTGGTT	CTGCCGGTGG
1010	1020	1030	1040	1050
TCGGGCCGCC	GTCCACGTGC	TGCAAGGTGG	AGGCGAGCGC	GGTTGAGAAG
1060	1070	1080	1090	1100
GCAGAAGAGT	TTGCCGCCAA	CAAGGAGCTG	TCCGTCTAAC	AGCCGGACGA
1110	1120	1130	1140	1150
TCGAAAGGCG	CACTATATTA	TGGCAATAAA	TCATTTGATT	ATACTTATGC
1160	1170	1180	1190	1200
TGCATTTGCG	AAGCTAAGGT	ATACTATGCA	AGCCATATGT	TTGTGTTTCGT
1210	1220	1230	1240	1250
ACGTGTTGTT	TGGGACGTAC	AGTTGTGTTG	TTGTACGTCG	TGAAGTACTG
1260	1270	1280	1290	1300
AAGTGTTTAC	AGTAGATCAC	AAGTTCACAG	CAATCAATGA	GGACCCTGTA
1310	1320	1330	1340	1350
AGCCAGTGTA	AACGAGGAAC	ATGCCATCTG	TGTATGACAG	TGAGAAATTA
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<210> 17

<211> 320

<212> PRT

<213> *Arabidopsis thaliana*

<400> 17

Met Ala Cys Gln Asn Asn Leu Val Val Lys Gln Ile Ile Asp Leu

15

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Val Asp Thr Leu Phe Gly Gln Leu Val Ser Thr Cys Leu Pro Thr	45
Asp Thr Asn Ile Asp Val Thr Asn Met Cys Glu Glu Val Lys Asp	60
Met Arg Ala Asn Leu Ile Lys Leu Cys Gly Glu Ala Glu Gly Tyr	75
Leu Glu Gln His Phe Ser Thr Ile Leu Gly Ser Leu Gln Glu Asp	90
Gln Asn Pro Leu Asp His Leu His Ile Phe Pro Tyr Tyr Ser Asn	105
Tyr Leu Lys Leu Gly Lys Leu Glu Phe Asp Leu Leu Ser Gln His	120
Ser Ser His Val Pro Thr Lys Ile Ala Phe Val Gly Ser Gly Pro	135
Met Pro Leu Thr Ser Ile Val Leu Ala Lys Phe His Leu Pro Asn	150
Thr Thr Phe His Asn Phe Asp Ile Asp Ser His Ala Asn Thr Leu	165
Ala Ser Asn Leu Val Ser Arg Asp Pro Asp Leu Ser Lys Arg Met	180
Ile Phe His Thr Thr Asp Val Leu Asn Ala Thr Glu Ala Leu Asp	195
Gln Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Asp Lys	210
Glu Ser Lys Val Lys Ala Ile Glu His Leu Glu Lys His Met Ala	225
Pro Gly Ala Val Leu Met Leu Arg Arg Ala His Ala Leu Arg Ala	240
Phe Leu Tyr Pro Ile Val Asp Ser Ser Asp Leu Lys Gly Phe Gln	255
Leu Leu Thr Ile Tyr His Pro Thr Asp Asp Val Val Asn Ser Val	270
Val Ile Ala Arg Lys Leu Gly Gly Pro Thr Thr Pro Gly Val Asn	285
Gly Thr Arg Gly Cys Met Phe Met Pro Cys Asn Cys Ser Lys Ile	300
His Ala Ile Met Asn Asn Arg Gly Lys Lys Asn Met Ile Glu Glu	315
Phe Ser Thr Ile Glu	320

<210> 18

<211> 963

<212> DNA

<213> *Arabidopsis thaliana*

<400> 18

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ACGTGCTTAC CCACGGATAC AAACATCGAT GTCACAAATA TGTGTGAAGA AGTCAAAGAC	180
ATGAGAGCTA ATCTCATCAA GCTTTGTGGT GAAGCCGAAG GTTATTTGGA GCAACACTTC	240
TCCACAATTT TGGGATCTTT ACAAGAAGAC CAAAACCCAC TTGACCATTT ACACATCTTT	300
CCTTACTACT CCAACTACCT CAAGCTAGGC AAGCTCGAGT TCGATCTCCT GAGCCAACAC	360
TCAAGCCATG TCCCCACCAA GATTGCCTTC GTGGGTTTCGG GTCCGATGCC TCTCACATCC	420
ATCGTATTGG CCAAGTTTCA CCTCCCCAAC ACGACGTTCC ACAACTTTGA CATCGACTCA	480
CACGCAAACA CACTCGCTTC AAACCTCGTC TCTCGCGACC CGGACCTCTC AAAACGCATG	540
ATCTTCCACA CAACGGACGT ACTAAACGCA ACCGAAGCCC TTGACCAATA TGACGTCGTT	600
TTCTTAGCGG CGCTTGTAGG GATGGACAAA GAGTCAAAGG TCAAAGCCAT CGAGCACTTG	660
GAGAAACACA TGGCTCCTGG AGCTGTTCTT ATGCTAAGGA GGGCTCATGC TCTCAGAGCT	720
TTCTTATATC CAATCGTTGA CTCGTCTGAT CTCAAAGGCT TTCAACTCTT GACCATCTAT	780
CATCCAACCG ATGACGTGGT TAACTCGGTT GTGATCGCAC GTAAGCTCGG TGGTCCGACC	840
ACGCCCCGGG TTAATGGTAC TCGTGGATGC ATGTTTATGC CTTGTAAGTGT CTCCAAGATT	900
CACGCGATCA TGAACAACCG TGGTAAGAAG AATATGATCG AGGAGTTTAG TACCATCGAG	960
TAA	963

<210> 19

<211> 320

<212> PRT

<213> *Arabidopsis thaliana*

<400> 19

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Tyr Asn Gln Ile Ser Asn Leu Glu Ser Leu Lys Pro Ser Lys Asn	30
Val Asp Thr Leu Phe Arg Gln Leu Val Ser Thr Cys Leu Pro Thr	45
Asp Thr Asn Ile Asp Val Thr Glu Ile His Asp Glu Lys Val Lys	60
Asp Met Arg Ser His Leu Ile Lys Leu Cys Gly Glu Ala Glu Gly	75
Tyr Leu Glu Gln His Phe Ser Ala Ile Leu Gly Ser Phe Glu Asp	90

Asn Pro Leu Asn His Leu His Ile Phe Pro Tyr Tyr Asn Asn Tyr	105
Leu Lys Leu Gly Lys Leu Glu Phe Asp Leu Leu Ser Gln His Thr	120
Thr His Val Pro Thr Lys Val Ala Phe Ile Gly Ser Gly Pro Met	135
Pro Leu Thr Ser Ile Val Leu Ala Lys Phe His Leu Pro Asn Thr	150
Thr Phe His Asn Phe Asp Ile Asp Ser His Ala Asn Thr Leu Ala	165
Ser Asn Leu Val Ser Arg Asp Ser Asp Leu Ser Lys Arg Met Ile	180
Phe His Thr Thr Asp Val Leu Asn Ala Lys Glu Gly Leu Asp Gln	195
Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Asp Lys Glu	210
Ser Lys Val Lys Ala Ile Glu His Leu Glu Lys His Met Ala Pro	225
Gly Ala Val Val Met Leu Arg Ser Ala His Gly Leu Arg Ala Phe	240
Leu Tyr Pro Ile Val Asp Ser Cys Asp Leu Lys Gly Phe Glu Val	255
Leu Thr Ile Tyr His Pro Ser Asp Asp Val Val Asn Ser Val Val	270
Ile Ala Arg Lys Leu Gly Gly Ser Asn Gly Ala Arg Gly Ser Gln	285
Ile Gly Arg Cys Val Val Met Pro Cys Asn Cys Ser Lys Val His	300
Ala Ile Leu Asn Asn Arg Gly Met Glu Lys Asn Leu Ile Glu Glu	315
Phe Ser Ala Ile Glu	320

<210> 20

<211> 963

<212> DNA

<213> *Arabidopsis thaliana*

<400> 20

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ACGTGCTTAC CAACGGACAC GAACATCGAT GTCACAGAGA TACACGATGA AAAAGTCAAA	180
GACATGAGAT CTCATCTCAT CAAGCTTTGT GGTGAAGCCG AAGGTTATTT AGAGCAACAC	240
TTTTCAGCAA TCTTAGGCTC TTTTGAAGAC AACCTCTAA ACCATTTACA CATCTTCCCC	300

TATTACAACA ACTATCTCAA ACTAGGCAAA CTCGAATTCG ATCTCCTTTC TCAGCACACA	360
ACCCATGTCC CGACCAAAGT CGCCTTTATT GGTTCGGGTC CGATGCCACT TACTTCCATC	420
GTCTTGGCCA AGTTCCACCT CCCC AACACA ACGTTCCACA ACTTCGACAT CGACTCACAC	480
GCCAACACAC TCGCTTCAAA CCTCGTTTCT CGTGATTCTG ACCTTTCCAA ACGCATGATT	540
TTCCACACAA CTGATGTATT AAACGCTAAG GAGGGGTTAG ACCAATACGA TGTGTGTTTC	600
TTGGCAGCTC TTGTTGGGAT GGATAAAGAG TCAAAGGTCA AAGCTATTGA GCATTTAGAG	660
AAGCATATGG CCCCTGGAGC TGTGGTGATG CTAAGAAGTG CTCATGGTCT TAGAGCTTTC	720
TTGTATCCAA TCGTTGACTC TTGTGATCTT AAAGGGTTTG AGGTGTAAAC CATTTATCAT	780
CCGTCTGACG ACGTGGTTAA TTCGGTGGTC ATCGCACGTA AGCTTGGTGG TTCAAATGGA	840
GCTCGAGGCA GCCAGATCGG ACGGTGTGTG GTTATGCCTT GTAATTGCTC TAAGGTCCAC	900
GCGATCTTGA ACAATCGTGG TATGGAGAAG AATTTGATCG AGGAGTTTAG TGCCATCGAG	960
TAA	963

<210> 21

<211> 320

<212> PRT

<213> *Arabidopsis thaliana*

<400> 21

Met Gly Cys Gln Asp Glu Gln Leu Val Gln Thr Ile Cys Asp Leu	15
Tyr Glu Lys Ile Ser Lys Leu Glu Ser Leu Lys Pro Ser Glu Asp	30
Val Asn Ile Leu Phe Lys Gln Leu Val Ser Thr Cys Ile Pro Pro	45
Asn Pro Asn Ile Asp Val Thr Lys Met Cys Asp Arg Val Gln Glu	60
Ile Arg Leu Asn Leu Ile Lys Ile Cys Gly Leu Ala Glu Gly His	75
Leu Glu Asn His Phe Ser Ser Ile Leu Thr Ser Tyr Gln Asp Asn	90
Pro Leu His His Leu Asn Ile Phe Pro Tyr Tyr Asn Asn Tyr Leu	105
Lys Leu Gly Lys Leu Glu Phe Asp Leu Leu Glu Gln Asn Leu Asn	120
Gly Phe Val Pro Lys Ser Val Ala Phe Ile Gly Ser Gly Pro Leu	135
Pro Leu Thr Ser Ile Val Leu Ala Ser Phe His Leu Lys Asp Thr	150

Ile Phe His Asn Phe Asp Ile Asp Pro Ser Ala Asn Ser Leu Ala	165
Ser Leu Leu Val Ser Ser Asp Pro Asp Ile Ser Gln Arg Met Phe	180
Phe His Thr Val Asp Ile Met Asp Val Thr Glu Ser Leu Lys Ser	195
Phe Asp Val Val Phe Leu Ala Ala Leu Val Gly Met Asn Lys Glu	210
Glu Lys Val Lys Val Ile Glu His Leu Gln Lys His Met Ala Pro	225
Gly Ala Val Leu Met Leu Arg Ser Ala His Gly Pro Arg Ala Phe	240
Leu Tyr Pro Ile Val Glu Pro Cys Asp Leu Gln Gly Phe Glu Val	255
Leu Ser Ile Tyr His Pro Thr Asp Asp Val Ile Asn Ser Val Val	270
Ile Ser Lys Lys His Pro Val Val Ser Ile Gly Asn Val Gly Gly	285
Pro Asn Ser Cys Leu Leu Lys Pro Cys Asn Cys Ser Lys Thr His	300
Ala Lys Met Asn Lys Asn Met Met Ile Glu Glu Phe Gly Ala Arg	315
Glu Glu Gln Leu Ser	320

<210> 22

<211> 963

<212> DNA

<213> Arabidopsis thaliana

<400> 22

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ACATGCATAC CACCAAACCC TAACATCGAT GTCACCAAGA TGTGTGACAG AGTCCAAGAG	180
ATTCGACTTA ATCTCATCAA GATTTGTGGT CTAGCCGAAG GTCACCTAGA AAACCATTTC	240
TCTTCGATCT TGACCTCTTA CCAAGACAAC CCACTTCATC ATTTAAACAT TTTCCCTTAT	300
TACAACAACCT ATTTGAAACT CGGAAAGCTC GAGTTCGACC TCCTCGAACA AAACCTAAAT	360
GGCTTTGTCC CAAAGAGTGT GGCTTTTCATT GGATCTGGTC CTCTTCCTCT CACTTCCATC	420
GTTCTTGCTT CATTCCATCT CAAAGACACA ATCTTTCACA ACTTTGACAT CGACCCATCA	480
GCGAACTCAC TCGCTTCTCT TCTGGTTTCC TCTGATCCAG ACATCTCTCA ACGCATGTTC	540
TTCCACACCG TTGATATAAT GGACGTGACA GAGAGCTTAA AGAGCTTTGA TGTCGTGTTT	600

CTAGCTGCTC TTGTTGGAAT GAACAAAGAG GAGAAAGTTA AAGTGATCGA GCATCTGCAG	660
AAACACATGG CTCCTGGTGC TGTGCTCATG CTTAGGAGTG CTCATGGTCC GAGAGCGTTT	720
CTTTATCCGA TCGTTGAGCC GTGTGATCTT CAGGGGTTTCG AGGTTTTGTC TATTTATCAC	780
CCAACAGATG ATGTTATCAA CTCCGTGGTG ATCTCTAAAA AGCATCCAGT TGTTTCAATT	840
GGGAATGTTG GTGGTCCTAA TTCATGCTTG CTCAAGCCTT GCAACTGTTC CAAGACCCAC	900
GCGAAAATGA ACAAGAACAT GATGATCGAG GAGTTCGGAG CTAGGGAGGA ACAGTTGTCT	960
TAA	963